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APPLICATION NO. FILING DATE		LING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/019,219 12/28/2001		Christophe Ronsin	065691-0263	1844	
22428	7590	08/25/2003			
FOLEY AN	D LARI	ONER	EXAMINER		
SUITE 500			NICKOL, GARY B		
3000 K STRE		****	Mokob, GART B		
WASHINGTON, DC 20007				ART UNIT	PAPER NUMBER
				1642	11
				DATE MAILED: 08/25/2003	1/

Please find below and/or attached an Office communication concerning this application or proceeding.

		Application No.	Applicant(s)	_				
		10/019,219	RONSIN ET AL.					
	Office Action Summary	Examiner	Art Unit	_				
		Gary B. Nickol Ph.D.	1642					
	- The MAILING DATE of this communication app	ears on the cover shee	t with the correspondence address					
Period for Reply								
A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION. - Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication. - If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely. - If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication. - Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). - Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).								
Status								
·	1) Responsive to communication(s) filed on 25 June 2003.							
2a)☐	,	s action is non-final.						
3)∟_	3) Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under Ex parte Quayle, 1935 C.D. 11, 453 O.G. 213.							
Dispositi	on of Claims		,					
4)⊠	4)⊠ Claim(s) <u>1-36</u> is/are pending in the application.							
	4a) Of the above claim(s) 6,9-16,18-20 and 24-36 is/are withdrawn from consideration.							
	5) Claim(s) is/are allowed.							
	Claim(s) <u>1-5,7,8,17 and 21-23</u> is/are rejected.							
·	Claim(s) is/are objected to.							
	Claim(s) are subject to restriction and/or papers	election requirement.						
	The specification is objected to by the Examiner		·					
	The drawing(s) filed on is/are: a) accep		by the Examiner					
. 5/	Applicant may not request that any objection to the	• == •	•					
11) 🔲 7	The proposed drawing correction filed on							
	If approved, corrected drawings are required in rep							
12)☐ The oath or declaration is objected to by the Examiner.								
Priority u	nder 35 U.S.C. §§ 119 and 120		·					
13)⊠	13) Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).							
a)[a) ☐ All b) ☐ Some * c) ☐ None of:							
	1. Certified copies of the priority documents have been received.							
	2. Certified copies of the priority documents have been received in Application No							
	 3. Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)). * See the attached detailed Office action for a list of the certified copies not received. 							
14) Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).								
a) ☑ The translation of the foreign language provisional application has been received. 15) ☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.								
Attachment		- -						
2) Notice	e of References Cited (PTO-892) e of Draftsperson's Patent Drawing Review (PTO-948) nation Disclosure Statement(s) (PTO-1449) Paper No(s) <u>3</u> .	5) Notice	ew Summary (PTO-413) Paper No(s) of Informal Patent Application (PTO-152)					

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DETAILED ACTION

The Election filed June 25, 2003 (Paper No. 10) in response to the Office Action of March 25, 2003 is acknowledged and has been entered.

Claims 1-36 are pending in the application.

Claims 6, 9-16, 18-20, and 24-36 have been withdrawn from further consideration by the examiner under 37 CFR 1.142(b) as being drawn to non-elected inventions.

Claims 1-5, 7-8, 17, and 21-23 are currently under prosecution.

Applicant's election with traverse of Group 1, claims 1-5, 7-8, 17, and 21-23 in Paper No 10 is acknowledged. The traversal is on the ground(s) that Group 1 and Group 3 should be examined together since Group 3 includes claims drawn to DNA encoding the peptides of Group 1. This argument has been considered but is not found persuasive. Although Example 17 of the administrative instructions indicates that peptides and DNA encoding said peptides exhibit corresponding special technical features, the claims of the instant application are broader and include multiple special technical features encompassing multiple products and multiple processes of use for the reasons set forth in Paper No. 8. Hence, only one product and one process of use of said product relate to a single general inventive concept. Thus, since the DNA of Group 3 is not used in the method of Claim 4, there is not special technical feature linking the products of Group 3 to the *general* inventive concept that encompasses the method of Claim 4. Applicants further note that Groups 6 through 10 are drawn to uses of the product of Group 1 and that once the product of Group 1 is found to be allowable the claims encompassed by Groups 6

through 10 must be rejoined and examined. This assertion is noted. Applicants are advised that rejoinder will be considered provided that the use claims contain the same limitations as the corresponding allowed product claims. For these reasons the restriction requirement is deemed to be proper and is therefore made FINAL.

Specification

The specification is objected to because it contains an embedded hyperlink and/or other form of browser-executable code (i.e., see pages 3 and 5). See MPEP §608.01. Examples of a hyperlink or a browser-executable code are a URL placed between these symbols "<>" and http:// followed by a URL address. Merely deleting said symbols and " http:// " would obviate this objection. Patent publications of website addresses are permitted, but direct linkage to said sites must be disabled since USPTO policy does not permit the USPTO to link to any commercial sites since the USPTO exercises no control over the organization, views or accuracy of the information contained on these outside sites.

The specification is further objected to for improper disclosure of amino acid sequences without reference to a sequence identifier (See Figure 5, recitation of "VISTVVANL" does not include a SEQ ID NO.) Thus, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825. This definition sets forth limits, in terms of numbers of amino acids and/or numbers of nucleotides, at or above which compliance with the sequence rules is required.

Amino acid sequences as used in 37 CFR 1.821 through 1.825 are interpreted to mean an unbranched sequence of four or more amino acids. If, these sequence represent portions of

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sequences which have been previously disclosed in a computer readable file (CRF), applicant can amend the specification, *for example*, to read "VISTVVANL", amino acids 1-9 of SEQ ID NO:21. If, however, these sequences have not been previously disclosed in a CRF, applicant **must** provide a computer readable form (CRF) of the sequence listing, an initial or substitute paper copy of the sequence listing, as well as any amendment directing its entry into the specification, and a statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e-f) or 1.825(b) or 1.825(d).

Claim Objections

Claims 7-8 are objected to as being dependent from non-elected subject matter, i.e. claim 7, line 2 recites "as claimed in claim 6".

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1-3, 5, and 7-8 as written, do not sufficiently distinguish over peptides as they exist naturally because the claims do not particularly point out any non-naturally occurring differences between the claimed products and the naturally occurring products. In the absence of the hand of man, the naturally occurring products are considered non-statutory subject matter. See Diamond v. Chakrabarty, 447 U.S. 303, 206 USPQ 193 (1980). The claims should be

amended to indicate the hand of the inventor, e.g., by insertion of "recombinant" as taught by page 24, lines 25-32 of the specification. See MPEP 2105.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Regarding claims 4-5, the phrase "preferably" in Claim 4 renders the claims indefinite because it is unclear whether the limitation(s) following the phrase are part of the claimed invention. See MPEP § 2173.05(d).

Claims 4-5 are rejected under 35 U.S.C. 112, second paragraph, as being incomplete for omitting essential steps, such omission amounting to a gap between the steps. See MPEP § 2172.01. The omitted step is: a correlation step describing how the results of the assay relate back to the preamble of the method.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-3 and 7-8 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a recombinant peptide comprising SEQ ID NO. 1 or a recombinant peptide consisting of SEQ ID NO:2 does not reasonably provide enablement for the

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broadly claimed peptide compounds. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention commensurate in scope with these claims.

Factors to be considered in determining whether undue experimentation is required, are summarized in *Ex parte* Forman, 230 USPQ 546 (BPAI 1986). They include the nature of the invention, the state of the prior art, the relative skill of those in the art, the amount of direction or guidance disclosed in the specification, the presence or absence of working examples, the predictability or unpredictability of the art, the breadth of the claims, and the quantity of experimentation which would be required in order to practice the invention as claimed.

The claims are broadly drawn to peptide compounds of at least 8 consecutive amino acids of SEQ ID NO:1 that cause a specific T cell response. The claims are further limited to the peptides of Claim 1 that comprise at least 80% identity with the sequence of SEQ ID NO:2 or peptides that comprises at least one element other than natural amino acids. The claims are further drawn to peptide compounds comprising a sequence of approximately 9 to 10 amino acids of SEQ ID NO:1 which has at least one mutation or one modification which respect to the sequence of SEQ ID NO:1, and which further causes a specific T response. The claims are further drawn to a peptide compound as claimed in Claim 7, characterized in that it is derived from SEQ ID NO:2.

This includes an infinite number of peptides which have 8 consecutive amino acids of SEQ ID NO:1 or an infinite number of peptides comprising a sequence of approximately 9 to 10 amino acids of SEQ ID NO:1 which has at least one mutation or one modification which respect to the sequence of SEQ ID NO:1, and which further causes a specific T response.

The specification teaches (page 3) that SEQ ID NO:1 is a polypeptide of 162 amino acids. The specification further teaches that (page 6) the term "peptide compound" is intended to mean an entity which consists of a minimum of one peptide fragment derived from the polypeptide encoded by an A + 1 or A +2 alternative ORF of iCE, or of a series of said peptide fragments, and which optionally has one or more other elements other then natural or unnatural amino acids.

One cannot extrapolate the teachings of the specification to the scope of the claims because the claims are broadly drawn to any and all peptide fragments of 8 consecutive amino acids in length (or peptides comprising a sequence of approximately 9 to 10 amino acids of SEQ ID NO:1 which has at least one mutation or one modification) with or without the biological properties of what is claimed, and applicant has not enabled all of these types of modified peptides because it would not be expected nor could one predict that these modified peptides would be capable of functioning as that which is being disclosed. For example, the claims indicate that the peptide compounds of at least 8 consecutive amino acids of SEQ ID NO:1 cause a specific T cell response. However, the specification teaches (page 25) that after examining the corresponding amino acid sequence, "all possible nonamers and decamers were synthesized" were evaluated for their ability to make autologous EBV-transformed B cells sensitive to lysis. However, none of them proved to be positive. Only the nonamer (SPRWWPTCL) consisting of SEQ ID NO:2 achieved semi-maximum lysis of transformed B cells.

Further, those of skill in the art, recognize that protein chemistry is probably one of the most unpredictable areas of biotechnology. For example, conservative replacement of a single "lysine" reside at position 118 of acidic fibroblast growth factor by "glutamic acid" led to the

substantial loss of heparin binding, receptor binding and biological activity of the protein (Burgess et al., J of Cell Bio. 111:2129-2138, 1990). In transforming growth factor alpha, replacement of aspartic acid at position 47 with alanine or asparagine did not affect biological activity while replacement with serine or glutamic acid sharply reduced the biological activity of the mitogen (Lazar et al. Molecular and Cellular Biology 8:1247-1252, 1988). These references demonstrate that even a single amino acid substitution or what appears to be an inconsequential chemical modification will often dramatically affect the biological activity and characteristic of a protein. Furthermore, the specification fails to teach what deletions, truncations, substitutions and mutations of the disclosed sequence can be tolerated that will allow the protein to function as claimed. While it is known that many amino acid substitutions are possible in any given protein, the position within the protein's sequence where such amino acid substitutions can be made with reasonable expectation of success are limited. Certain positions in the sequence are critical to the three-dimensional structure/function relationship, and these regions can tolerate only conservative substitutions or no substitutions. Reasonable correlation must exist between the scope of the claims and scope of enablement set forth, and it cannot be predicted from the disclosure how to use any and all such peptide compositions. Therefore, in view of the lack of predictability of the prior art, the breadth of the claims and the absence of working examples, it would require undue experimentation for one skilled in the art to use the invention as claimed.

Claims 4-5, 17, and 20-23 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

Factors to be considered in determining whether undue experimentation is required, are summarized in *Ex parte* Forman, 230 USPQ 546 (BPAI 1986). They include the nature of the invention, the state of the prior art, the relative skill of those in the art, the amount of direction or guidance disclosed in the specification, the presence or absence of working examples, the predictability or unpredictability of the art, the breadth of the claims, and the quantity of experimentation which would be required in order to practice the invention as claimed.

The claims are broadly drawn to a method for identifying peptide compounds comprising a sequence which has at least 80% identity with a sequence of approximately 9 to 10 consecutive amino acids of SEQ ID NO:1 comprising a) determining fragments which possess a sequence of approximately 9 to 10 amino acids comprising an anchoring motif for a given HLA molecule, b) determining the immunogenicity of the peptide fragments obtained in step a), preferably by carrying out an Elispot assay. The claims are further drawn to a peptide compound which can be obtained using a method as claimed in Claim 4. The claims are further drawn to pharmaceutical compositions comprising a peptide compound or a mixture of peptide compounds as claimed in Claim 1.

The claims are not enabled because the specification fails to provide reasonable guidance and objective evidence that one of skill in the art would know how to use the method in any predictable manner or to use the obtained peptides in any predictable manner, or to use the pharmaceutical compositions in any predictable manner.

With regards to methods of identifying peptides, the specification teaches (page 4) that the peptide fragments to be assayed can be easily obtained by chemical synthesis. The specification further teaches that immunogenicity can be determined by Elispot assays which is

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widely known in the art. However, the specification fails to provide reasonable guidance that random synthesis of an infinite number of such peptides through trial and error would provide one of ordinary skill in the art a reasonable expectation of success that such peptides would be immunogenic as determined by Elispot assays. Thus, the claims are broadly seeking protection for any and all potentially immunogenic peptides through trial and error and the specification has failed to teach a reasonable expectation of success that all such peptides would be immunogenic through Elispot assays. Further, the specification teaches (page 25) that after examining the corresponding amino acid sequence, "all possible nonamers and decamers were synthesized" and were evaluated for their ability to make autologous EBV-transformed B cells sensitive to lysis. However, none of them proved to be positive. Only the nonamer (SPRWWPTCL) consisting of SEQ ID NO:2 achieved semi-maximum lysis of transformed B cells. The specification further teaches that this nonamer comprises HLA-B7 anchoring residues in positions 2, 3, and 9. Thus, it would appear that the method is not enabled because it broadly calls for identifying an infinite number of peptide fragments of approximately 9 to 10 amino acids long comprising an anchor motif for any given HLA molecule, and the specification fails to teach how one of ordinary skill in the art would predictably practice the method as claimed or how to use any and all such peptides in any manner consistent with the teachings of the specification.

Further, the claims are not enabled for pharmaceutical compositions. The specification teaches (page 12, line 19) that the alternative open reading frame of iCE expresses a novel tumor antigen which is advantageous for use in immunotherapy, in particular in patients with a hepatocarcinoma or adenocarinoma of the colon or of the kidney. However, the specification does not provide sufficient guidance and or objective evidence that such a pharmaceutical

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composition would predictably and effectively function as claimed. Bellone *et al.* . (Immunology Today, v20 (10), 1999, pp.457-462) summarize the current state of the art of peptide immunotherapy including clinical trials where "there is usually a poor correlation between induction of specific T-cells and the clinical responses" (page 457, 2nd column). Bellone *et al.* teach the disadvantages of peptide cancer immunotherapy in that (1) there is no direct evidence for a role in tumor rejection, (2) the therapy is applicable to few patients, (3) risk of generating tumor escape mutants, and (4) risk of autoimmune reactions (page 461, Box 1). Further, Anderton, S. (Immunology, Vol. 104, pages 367-376, 2001) teach (page 370, 2nd column) that altered peptide ligand (APL) therapy is complicated by a multitude of factors including a) the complexity of the T-cell repertoire; b) the unpredictability of the effects of APL; and c) harmful hyper-reactivity to the APL. All of this underscores the criticality of providing workable examples which is not disclosed in the specification, particularly in an unpredictable art, such as immunotherapy of cancer.

In view of the teachings above, and the lack of guidance and or exemplification in the specification, it would not be predictable for of skill in the art to use the pharmaceutical compositions or vaccine formulations as contemplated in the disclosure. Thus, it would require undue experimentation by one of skill in the art to practice the invention as claimed.

Claims 1-5, 7-8, 17, and 21-23 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

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The claims are broadly drawn to peptide compounds of at least 8 consecutive amino acids of SEO ID NO:1 that cause a specific T cell response. The claims are further limited to the peptides of Claim 1 that comprise at least 80% identity with the sequence of SEQ ID NO:2 or peptides that comprises at least one element other than natural amino acids. The claims are further drawn to peptide compounds comprising a sequence of approximately 9 to 10 amino acids of SEQ ID NO:1 which has at least one mutation or one modification which respect to the sequence of SEO ID NO:1, and which further causes a specific T response. The claims are further drawn to a peptide compound as claimed in Claim 7, characterized in that it is derived from SEO ID NO:2. The claims are also drawn to a method for identifying peptide compounds comprising a sequence which has at least 80% identity with a sequence of approximately 9 to 10 consecutive amino acids of SEO ID NO:1 comprising a) determining fragments which possess a sequence of approximately 9 to 10 amino acids comprising an anchoring motif for a given HLA molecule, b) determining the immunogenicity of the peptide fragments obtained in step a), preferably by carrying out an Elispot assay. The claims are further drawn to a peptide compound which can be obtained using a method as claimed in Claim 4. The claims are further drawn to pharmaceutical compositions comprising a peptide compound or a mixture of peptide compounds as claimed in Claim 1. The claims do not require that the polypeptide or the method possess any particular conserved structure, or other disclosed distinguishing feature. Thus, the claims are drawn to obtaining a genus of peptide compounds. However, the written description in this case only sets forth a recombinant peptide comprising SEQ ID NO:1 and a recombinant peptide consisting of SEQ ID NO:2 and therefore the written description is not commensurate in scope with the claims which read on an infinite number of variant peptides.

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To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, the only factor present in the claim is a partial structure (SEQ ID NO:2) that appears to make autologous EBV-transformed B cells sensitive to lysis (page 25). Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus.

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the 'written description' inquiry, whatever is now claimed." (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See Vas-Cath at page 1116). As discussed above, the skilled artisan cannot envision the detailed chemical structure of the encompassed genus of polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See Fiers v. Revel, 25 USPQ2d 1601 at 1606 (CAFC 1993) and Amgen Inc. v. Chugai Pharmaceutical Co. Ltd., 18 USPQ2d 1016.

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One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Therefore, only a recombinant peptide comprising SEQ ID NO:1 and a recombinant peptide consisting of SEQ ID NO:2, but not the full breadth of the claims meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 7-8 are rejected under 35 U.S.C. 102(b) as being anticipated by Kato *et al.* (PIR Database, Accession No. JQ0137, 1996).

The claims are broadly interpreted to include any and all peptide compounds that possess any 9 to 10 amino acids of SEQ ID NO:1 in any order including at least one mutation or modification with respect to SEQ ID NO:1. Further, a specific T response is broadly interpreted to include any immunological response including the elicitation of antibodies. Further, with

regards to Claim 8, a peptide compound that is *derived* from SEQ ID NO:2 is interpreted as any peptide compound that has any amino acid in common with SEQ ID NO:2.

Kato et al. teach a peptide compound that possess 9 to 10 amino acids of SEQ ID NO:1 including at least one mutation or modification with respect to SEQ ID NO:1. Kato et al. further teach that said peptide includes the amino acids (SPR-WP) which are derived from SEQ ID NO:2 (See attached sequence comparison). Although Kato et al. do not specifically teach that the peptide compound causes a specific T response, such a peptide would inherently elicit the production of antibodies for the purpose of generating polyclonal or monoclonal antibodies. Thus, the claimed peptide appears to be the same as the prior art. The office does not have the facilities and resources to provide the factual evidence needed in order to establish that the product of the prior art does not possess the same material, structural and functional characteristics of the claimed product. In the absence of evidence to the contrary, the burden is on the applicant to prove that the claimed product is different from those taught by the prior art and to establish patentable differences. See In re Best 562F.2d 1252, 195 USPQ 430 (CCPA 1977) and Ex parte Gray 10 USPQ 2d 1922 (PTO Bd. Pat. App. & Int. 1989).

No claim is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Gary B. Nickol Ph.D. whose telephone number is 703-305-7143. The examiner can normally be reached on M-F, 8:30-5:00 P.M..

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If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anthony Caputa can be reached on 703-308-3995. The fax phone numbers for the organization where this application or proceeding is assigned are 703-305-3014 for regular communications and 703-308-4242 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 703-308-0196.

Gary B. Nickol, Ph.D. Examiner
Art Unit 1642

GBN

August 21, 2003

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Gene 84, 31-38, 1989.
A;Title: Nucleotide sequence of a regulatory region controlling alginate synthesis in A;Reference number: JQ0132; MUID:90108714; PMID:2514124
A;Accession: JQ0137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U53341; PIDN:AAC69106.1; GSPDB:GN00028; CESP:F49E10.2
A;Experimental source: strain Bristol N2; clone F49E10
C;Genetics:
                                                                                                                                                                                                                                                                              hypothetical protein APE2332 - Aeropyrum pernix (strain KI)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: H72460
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JQ0137
hypothetical 30.1K protein – Pseudomonas aeruginosa
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                                                                                                                           A; Molecule type: DNA
A; Residues: 1-210 <KAW>
                                                                                                                                                                              A; Reference number:
A; Accession: H72460
                                                                                                                                                                                               A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                     DNA Res. 6, 83-101, 1999
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                                                                                          A; Experimental source:
                                                                                                              A;Cross-references:
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;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Jun-1996
;Accession: JQ0137
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                      Match
                                                         APE2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STSTTTTTTTSTATTTPQPTTTTTSEK------PVTLTTQTWTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSW-----RV---AWPSCPASLPA-QLMSSPRWWPTCLPVTKLTLRPWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPQRSQQERWRAWLRQVSRLRVSP--QAWPPVSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STQPATGATWTKWLHYAGSSRISPTLEATLTVSPFLASLRVARVCLRLLCPPYPKDSSTE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCLRLLCPPYPKDSSTEPSWRVAWPSCPASLPAQLMSSPRWWPTCLPVTKLTLRPWW
                                                                                                                                                                                                                                                                                                                                                                                                                                 PAWLQASRPRVSPHAWP---PAWLRASRLRFSPRAWP---PVSPQASPPAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51/1; 92/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-261 <KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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     Similarity
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                                                                                          DDBJ:AP000064;
ce: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176/3; 235/3; 332/2; 514/1; 543/2; 569/3; 677/1; 732/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.6%; Score 87.5;
24.8%; Pred. No. 2
   9.3%;
                                                                                                                                                                                                                                                  Horikawa, H.; Ya, S.; Funahashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 85.5;
Pred. No. 1
   Score
Pred.
                                                                                                          NID:g5105945; PIDN:BAA81344.1; PID:d1045130;
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   84.5;
No. 1.
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i, T.; Tanaka,
DB . 4;
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N-acetylglucosamine-specific receptor 1 precursor - human (;Species: Homo sapiens (man) (c;Species: Homo sapiens (man) (c;Date: 28-oct-1994 #sequence_revision 28-oct-1994 #text_change 17-Mar-1999 (c;Accession: A54770; S37024

Mziaut,

Η.;

Darbon,

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Mattei,

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Miquelis,

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A54770

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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.; submitted to GenBank, June 2000
A,Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.V.; Martins, C.A.; Miyaki, C. A.Authors: Martins, E.M.F.; Matsukuma, A.V.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa, A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Sawa, A.J. de M.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; anonymous, The Xylella fastidiosa Consortium of the Nature 406, 151-157, 2000\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           general secretory pathway protein L XF1524 [imported] - Xylella fastidiosa (strain
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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A;Exper1mental source: strain 9a5c
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105
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                                                                                                            63
                                                                                                                                                                71
                                                                                                                                                                                                                      12 WWGS-----LRW----FGVSIAPGVGGFWHWWWQSLLAWLPMRCRVQMGLLSERLLLSLQ
                                                                                                                                                                                                                                                                          25 WWSSSSTAWVSWASSALETSTQPATGATWTKWLH-----
                                                                                                                                                                                                                                                                                                                                                          Local
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                                                WWPTCLPVTKLTLRPWWAACGA 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ARVCLRLLCPPYPKDSST---EPSWRVAWPSCPASLPAQLMSSPRWWPTCLPVTKLTLR 140
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HW--LLPATSALCRPLRLPAGA 124
                                                                                                                                                                ATLTVSPFLASLRVARVCLRLLCPPYPKDSSTEPSWRVAWPSCPASLPAQLMSS----
                                                                                                          AD-----GLHLVRQCGDVL----
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                                                                                                                                                                                                                                                                                                                                                       Score 83.5;
Pred. No. 3
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                                                                                                          EPLVQVPWPITPQELSGMLLPKLQILPR
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